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this analysis, different numbers of PCR cycles (21, 23, 25 and 27) were used for the first PCR amplification whereas the second, nested PCR amplification using nPCR1 and nPCR2 as primers proceeded with 12 cycles for all samples.

PCR primer for first amplification:PCR1, CTAATACGACTCACTATAGGGC (SEQ ID NO:14)

PCR primer pair for second, nested amplification:

nPCR1, TCGAGCGGCCGCCCGGGCAGGT (SEQ ID NO:15)

nPCR2, AGCGTGGTCGCGGCCGAGGT (SEQ ID NO:16)

Please insert the enclosed paper copy of the Sequence Listing, page numbers 1-4, at the end of the application.

## **REMARKS**

Applicants request entry of this amendment in adherence with 37 C.F.R. § 1.821-1.825. This amendment is accompanied by a floppy disc containing the above named sequences, SEQ ID NOS:1-16, in computer-readable form, and a paper copy of the sequence information which has been printed from the floppy disc.

The information contained in the computer-readable disc was prepared through the use of the software program "PatentIn" and is identical to that of the paper copy. This amendment contains no new matter.

Attached hereto is a marked-up version of changes made to the specification by the amendment. The attachment is entitled <u>"VERSION WITH MARKINGS TO SHOW CHANGES MADE."</u>

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If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 650-326-2400.

Respectfully submitted,

Hugh Wang Reg. No. 47,163

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## **VERSION WITH MARKINGS TO SHOW CHANGES MADE**

Please amend Table IV, spanning pages 20-21, as follows:

Table IV

14010 1 4			
No	first adaptor	second adaptor	Corresponding primers
1*	5'-	5'-	5'-CTAATACGAC
	CTAATACGACTCACT	CTAATACGACTCA	TCACTATAGGGC-3'
	ATAGGGCTCGAGCGG	CTATAGGGCAGC	(SEQ ID NO:5);
	CCGCCCGGGCAGGT-3'	GTGGTCGCGGCC	
	(SEQ ID NO:1)	GAGGT-3'	Nested PCR Primer 1: 5'-
		(SEQ ID NO:3)	TCGAGCGGCCGCCGG
	5'- ACCTGCCCGG-3'		GCAGGT-3'
	(SEQ ID NO:2)	5'- ACCTCGGCCG-	(SEQ ID NO:6);
		3'	
		(SEQ ID NO:4)	Nested PCR Primer 2: 5'-
			AGCGTGGTCGCGGCCG
			AGGT-3
	*	,	(SEQ ID NO:7)
2*	5'-	5'-	5'-TCGAGCGGCCGCCC
	TCGAGCGGCCGCCG	AGCGTGGTCGCG	GGGCAGGT-3'
	GGCAGGT-3'	GCCGAGGT-3'	(SEQ ID NO:12)
	(SEQ ID NO:8)	(SEQ ID NO:10)	
			5'-AGCGTGGTCGCGGC
	5'- ACCTGCCCGG-3'	5'- ACCTCGGCCG-	CGAGGT-3'
	(SEQ ID NO:9)	3'	(SEQ ID NO:13)
ata		(SEQ ID NO:11)	
*nartially double-stranded			

<sup>\*</sup>partially double-stranded.

Please amend the paragraph beginning on page 49, line 31 as follows:

Following annealing, a 2-step (nested) PCR amplification was performed to isolate sequences of interest. In the first PCR reaction only molecules which different adapter sequences on each end are amplified exponentially by the adapter-specific primer PCR1. The number of PCR cycles needed to obtain sufficient amounts of amplicon for analysis depends on the experimental paradigm under investigation, and needs to be determined empirically by performing the PCR amplification procedure with different cycle numbers and analyzing amplicon yields (e.g., by agarose gel electrophoresis). In

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this analysis, different numbers of PCR cycles (21, 23, 25 and 27) were used for the first PCR amplification whereas the second, nested PCR amplification using nPCR1 and nPCR2 as primers proceeded with 12 cycles for all samples.

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